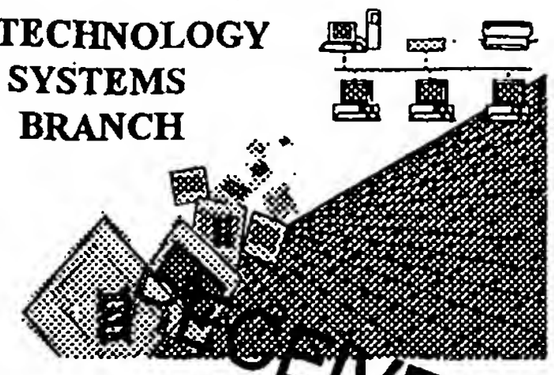
CRFI

BIOTECHNOLOGY SYSTEMS BRANCH



RECEIVED
AUG 11 2003
TECH CENTER 1600/2900

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/001,934A
Source: 1600
Date Processed by STIC: 8-4-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/001,934A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2_____	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3_____	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
4_____	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5_____	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,** each **n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6_____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7_____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8_____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9_____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10_____	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11 ✓	Use of <220>	Sequence(s) 21, 88, 94 that may be others missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12_____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13_____	Misuse of n	n can only be used to represent a single **nucleotide** in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

Does Not Comply
Corrected Diskette Needed

1600

RAW SEQUENCE LISTING DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:03

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

4 <110> APPLICANT: NAGY et al.
6 <120> TITLE OF INVENTION: HUMAN POLYPEPTIDES CAUSING OR LEADING TO THE KILLING
7 OF CELLS INCLUDING LYMPHOID TUMOR CELLS
9 <130> FILE REFERENCE: GPCG-P01-003
11 <140> CURRENT APPLICATION NUMBER: 10/001934A
12 <141> CURRENT FILING DATE: 2001-11-15
14 <150> PRIOR APPLICATION NUMBER: PCT/US01/15625
15 <151> PRIOR FILING DATE: 2001-05-14
17 <160> NUMBER OF SEQ ID NOS: 94
19 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

318 <210> SEQ ID NO: 21
319 <211> LENGTH: 10
320 <212> TYPE: PRT
321 <213> ORGANISM: artificial sequence
323 <220> FEATURE:
W--> 324 <221> NAME/KEY: MS-GPC8-6-VH-CDR3
325 <222> LOCATION: (1)..(10)
W--> 327 <223> OTHER INFORMATION:
W--> 327 <400> 21
329 Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr
E--> 330 1 5 **10**
2160 <210> SEQ ID NO: 88
2161 <211> LENGTH: 115
2162 <212> TYPE: PRT
2163 <213> ORGANISM: artificial sequence
2165 <220> FEATURE:
W--> 2166 <221> NAME/KEY: MS-GPC8-27-VL
2167 <222> LOCATION: (1)..(115)
W--> 2169 <223> OTHER INFORMATION:
W--> 2169 <400> 88
2170 Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
2171 1 5 10 15
2173 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
2174 20 25 30
2176 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
2177 35 40 45
2179 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
2180 50 55 60
2182 Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

See page 3

When using Artificial Sequence for numeric Identifier <213>. The Source of the genetic material must be marked in <223>. See Item # 11 on ERROR Summary SHEET.

Amino Acids should be numbered every 5.

Same as above. Note there may be others sequences with this problem. See page 3.

NO blank Spaces should be Included in numbering count.

RAW SEQUENCE LISTING DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:03

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

```
E--> 2183 65                  70                  75                  80
     2185 Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn
E--> 2186          85                  90                  95
     2188 Val His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
E--> 2189     100                 110                 115
     2364 <210> SEQ ID NO: 94
     2365 <211> LENGTH: 109
     2366 <212> TYPE: PRT
     2367 <213> ORGANISM: artificial sequence
     2369 <220> FEATURE:
W--> 2370 <221> NAME/KEY: MS-GPC8-27-41-VL
     2371 <222> LOCATION: (1)..(108)
W--> 2373 <223> OTHER INFORMATION:
W--> 2373 <400> 94
     2374 Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
     2375 1               5                   10                  15
     2377 Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
     2378             20                  25                  30
     2380 Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
     2381         35                  40                  45
     2383 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
     2384     50                  55                  60
     2386 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
     2387 65                  70                  75                  80
     2389 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
     2390                 85                  90                  95
     2392 His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
     2393          .  100                 105
E--> 2397 1
```

numbering must be every 5.

Same as first page see page 3

remove extra material at end of file.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:04

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or"Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29
Seq#:30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
Seq#:54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77
Seq#:78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94

VERIFICATION SUMMARY DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:04

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:60 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:63 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:artificial sequence
L:63 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:63
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:77 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:artificial sequence
L:77 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:77
L:87 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:artificial sequence
L:90 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:90
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:artificial sequence
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:103
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:118 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:artificial sequence
L:118 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:118
L:129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:132 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:artificial sequence
L:132 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:132
L:144 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:147 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:artificial sequence
L:147 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:147
L:159 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:162 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:artificial sequence
L:162 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:162
L:174 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:177 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:artificial sequence
L:177 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:177
L:189 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:artificial sequence
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:192
L:204 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:207 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:artificial sequence
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:207
L:218 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:221 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:artificial sequence
L:221 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:221
L:233 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15

L:236 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213> ORGANISM:artificial sequence
L:236 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:236
L:249 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:252 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213> ORGANISM:artificial sequence
L:252 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:252
L:264 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:267 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213> ORGANISM:artificial sequence

VERIFICATION SUMMARY DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:04

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

L:267 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:267
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:283 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:artificial sequence
L:283 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:283
L:294 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:297 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:artificial sequence
L:297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:297
L:308 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:311 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:artificial sequence
L:311 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:311
L:324 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:327 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:artificial sequence
L:327 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:327
L:330 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:339 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:342 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:artificial sequence
L:342 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:342
L:354 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:357 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:artificial sequence
L:357 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:357
L:369 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:372 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:artificial sequence
L:372 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:372
L:383 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:386 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:artificial sequence
L:386 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:386
L:397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:400 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:artificial sequence
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:400
L:412 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:415 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:artificial sequence
L:415 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:415
L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:442 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:457 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:471 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:485 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:501 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:516 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:531 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:545 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:559 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:574 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38

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L:588 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
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L:617 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:633 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42
L:648 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:663 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
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VERIFICATION SUMMARY DATE: 08/04/2003
PATENT APPLICATION: **US/10/001,934A** TIME: 07:19:04

Input Set : **N:\efs\10001934A\GPCG-P01-003SequenceListing.txt**
Output Set: **N:\CRF4\08012003\J001934A.raw**

L:678 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:692 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
L:707 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:721 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:736 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:751 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:2183 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:88
M:332 Repeated in SeqNo=88
L:2189 M:252 E: No. of Seq. differs, <211> LENGTH:Input:115 Found:109 SEQ:88
L:2397 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:94